

# SEQUENCE LISTING

## (1) GENERAL INFORMATION

- (i) APPLICANT: Cosgrove, Daniel, J.
- (ii) TITLE OF THE INVENTION: Beta-expansins as cell wall loosening agents, compositions thereof and methods of use
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Intellectual Property Office;  
The Pennsylvania State University
  - (B) STREET: 200 Innovation Boulevard, 113 Technology Center
  - (C) CITY: University Park
  - (D) STATE: PA
  - (E) COUNTRY: USA
  - (F) ZIP: 16802-7000
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 01-MAY-1998
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 60/045,445
  - (B) FILING DATE: 02-MAY-1997
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Thomas J. Monahan
  - (B) REGISTRATION NUMBER: 29,835
  - (C) REFERENCE/DOCKET NUMBER: 1564
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (814) 865-6279
  - (B) TELEFAX: (814) 865-3591
  - (C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 780 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCTTCCTCC	ACCTTCTAAT	AAGTGGCTCT	GGCTCTACTC	CACCGTTGAC	TCACTCCAAT	60
CAACAAGTGG	CAGCCACTCG	TTGGCTTCCC	GCCACCGCAA	CCTGGTACGG	AAGTGCCGAG	120
GGAGACGGCA	GCAGCGGAGG	AGCTTGTGGT	TACGGATCGT	TGGTGGACGT	GAAGCCGTTT	100
AAGGCTAGAG	TCGGAGCGGT	GAGTCCGATT	CTGTTCAAAG	GTGGTGAAGO	CTGCGGTGCA	240
TGCTACAAGG	TCAGGTGTCT	CGACAAGACC	ATTTGCTCTA	AGAGAGCAGT	CACCATTATT	300
GCCACCGACC	AGTCACCGTC	AGGACCATCT	GCTAAAGCAA	AACACACTCA	TTTCGACCTC	360
AGTGGCGCCG	CCTTTGGACA	TATGGCTATT	CCCGGCCATA	ACGGTGTCaT	CCGCAACCGT	420
GGCCTATTAA	ACATCCTCTA	CCGCCGAACG	GCATGCAAAT	ACAGAGGGAA	GAACATAGCG	480
TTTCATGTGA	ACGCAGGATC	AAGTGATTAT	TGGTTATCGC	TTCTCATTGA	GTATGAAGAC	540
GGTGAAGGAG	ACATTGGCTC	TATGCACATT	CGTCAAGCGG	GATCTAAGGA	GTGGATATCG	600
ATGAAGCACA	TATGGGGAGC	GAAGTGGTGC	ATCGTCGAAG	GACCACTCAA	GGGACCATTC	660
TCCGTGAAGC	TCACAACCTT	GTCCAACAAT	AAGACACTCT	CCGCCACCGA	CGTCATCCCC	720
AGTAACTGGG	TTCCCAAAGC	TACTTACACC	TCTCGCCTCA	ACTTCTCCCC	TGTTCTCTAA	780

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 999 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCACGCGTC	CGAGCAGACA	AGGTAGTAGT	ACAGOCTTTT	GTACGTACGT	AGCAGAGGGA	60
GTTCCCAAGA	TGGCTGGGGC	CTCTGCCAAG	GTCGTCGCGA	TGCTGCTCTC	CGTGCTCGCC	120
ACGTACGGCT	TCGCCGCCGG	CGTCGTCTAC	ACCAACGACT	GGCTCCCGGC	CAAGGCCACC	180
TGGTACGGCC	AGCCCAACGG	CGCCGGACCC	GACGACAACG	GCGGTGCGTG	CGGGTTCAAG	240
AACACCAACC	AGTACCCGTT	CATGTCCATG	ACCTCCTGCG	GCAACGAGCC	TCTGTTCCAG	300
GACGGCAAGG	GCTGTGGCGC	CTGCTACCAG	ATACGGTGCA	CCAACAACCC	GTCGTGCTCC	360
GGGCAGCCCC	GGACGGTGAT	CATCACGGAC	ATGAACTACT	ACCCCGTGCG	CAGGTACCAC	420
TTCCACCTGA	CGGCACGGC	GTTCCGGCCG	ATGGCGAGGC	CGGGGCTGAA	CGACCAGCTC	480
CGCCACGCCG	GCATCATCGA	CATCCAGTTC	AGGCGCGTCC	CGTGCTACCA	CCGCGGCCTC	540
TACGTGAACT	TCCACGTCGA	GGCCGGGTCC	AACCCGGTGT	ACCTCGCCGT	GCTGGTGGAG	600
TTCGCCAACA	AGGACGGCAC	GGTGGTGCAG	CTCGACGTCA	TGGAGTCGCT	CCCCAGCGGC	660
AAGCCGACGC	GGGTCTGGAC	GCCCATGCGC	CGCTCCTGGG	GATCCATCTG	GCGCCTCGAC	720
GCCAACCACC	GCCTCCAGGG	CCCCTTMTCC	CTCCGCATGG	TCAGCGAGTC	CGGCCAGACC	780
GTCATCGCCC	ACCAGGTCAT	CCCGGCCAAC	TGGAGGGCCA	ACACCAACTA	CGGCTCCAAA	840
GTCCAGTTCC	GTTGATCCAT	CGATCGATCT	ACCTATGTGC	ATGCAATGCC	TTCGTCGTCT	900
TGTGTCGCCG	GTCAAGAACG	AATTTTGATT	CTACCGATCG	GCAGTTCGGC	ACTAGTACTG	960
TACTACGATT	CTGTGTGTGT	GTGTGTGTGT	GTGTGATTG			999

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1004 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACGCGCTTAT	ACGATCATAT	AGGCGAATGG	GTACGGGCCC	CCCTCGAGGT	CGACCCACGC	60
GTCCGCGGTG	ATGTAGAGGT	AGTAGTGTA	TACCTGCTGC	TAGTATTAGT	GGTGGTGCAG	120
GGGTGCAAAG	GCAGCAGCGC	GGTGCAAGGT	GAAGGTCGGT	GGTACAACGA	GAGCGAGGCC	180
ATCGGTGGTG	CGGCGGCGTG	GGGGAACGCG	AAGGCGACGT	GGTACGGGCA	GCCGAACGGC	240
GCCGGGGCGG	CGGACAACGG	CGGGGCGTGC	GGGTTCAAGA	AGGTGAACCA	GTACCCGTTT	300
ATGGGGATGA	CGTCGTGCGG	GAACCASCCG	CTGTACAAGG	GCGGCAAGGG	CTGCGGCTCC	360
TGCTACCGCG	TCAGGTGCAA	TCGAAACCCC	GCCTGCTCCG	GCAACGCCCA	GACCGTCGCC	420
ATCAMCGACA	TGAACACTT	CCCCCTCTCC	CAGTACCACT	TCGACCTCAG	CGGCATCGCC	480
TTCGGCCGCC	TCGCCAAGCC	CGGCCGCGCC	GACGACCTCC	GCCGCGCGGG	GATCATCGAC	540
GTGCAGTTTC	CGCGCGTGCC	GTGCGAGTTC	CCGGGCCTCA	AGGTGGGATT	CCACGTGGAG	600
GAAGGTCCA	GCCCCGTGTA	CCTGGCGGTG	CTGGTGGAGT	ACGAGAACGG	CGACGGAGAC	660
GTGGCGCAGG	TGGACCTCAA	GGAGGCCGGC	GCCGGAGGAG	GAAGGTGGAC	GCCGATGCGG	720
GAGTCGTGGG	GGTCGGTGTG	GAGGCTGGAC	TCCAACCACC	GCCTGCGGGC	GCCATTCTCC	780
ATCCGCATCC	AGACGACTC	CGGCAAGACG	TTGGTGGCAC	CCGACGTCAT	CCCCCTCAAC	840
TGGACGCCCA	GCACCTTCTA	CCGTTCCCTT	GTCCAGTACT	CCTCCTAGCT	AGCTACTCCT	900
ATACCCATTA	ATTYTTCCCT	AATTATTCCT	TCTTGTTATT	ATATTCTACC	CTTATATATA	960
TATATATATA	TGTTATTAAA	AAAAAAAAAA	AAAAAAAAAA	AAAA		1004

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GACGCGCTAT	AGATCATATA	GGCGAATGGG	TACGGGCCCC	CCTCGAGGTC	GACCCACGCG	60
TCCGAAGCTC	AGAATCCTAC	CTGACTAGTA	CTACCACTAC	TAGCTAGTAG	CGAGCTACTC	120
TCTCTGGTCA	TCAAGCTTTG	AGTGGTTGGA	GTGGTGGCAG	CTATGGCTTT	TTCCATCTCC	180
AAGAAGGCTG	CAGTTGCTGC	ACTCTTCTCC	TTCTTTGTTG	TCACCTGCGT	CGCCGGCGCC	240
AGGCCGGGGA	ACTTCAGCGC	CTCCGACTTC	ACCGCCGATC	CCAAGTGGGA	AGTCGCCAGG	300
GCCACCTGGT	ACGGCGCTCC	CACCGCGGCC	GGCCCTGACG	ACGATGGCGG	TGCTTGCGGG	360
TTCAAGAACA	CCAACCAGTA	CCCGTTCTCG	TCGATGACCT	CCTGCGGCAA	CGAGCCTATC	420
TTCAAGGACG	GGAAGGGCTG	TGGCTCATGC	TACCAGATAA	GATGCGTCAA	CCACCCTGCC	480
TGCTCCGGCA	ACCCGGAGAC	GGTGATCATC	ACCGACATGA	ACTATACCCG	TTTCCAAGTA	540
CACTTCGACC	TGAGCGGCAC	GGCGTTCGGC	GCCATGGCCA	AGCCGGGGCA	GAACGACCAG	600
CTCCGCCACG	CCGGCATCAT	CGACATCCAG	TTCAAGAGGG	TGCCGTGCAA	CTTCCCTGGG	660
CTGAAGGTGA	CGTTCCACGT	GGAGGAGGGG	TCGAACCCGG	TGTACTTCGC	GGTGCTGGTT	720
GAGTACGAGG	ACGGCGACGG	CGACGTGGTG	CAGGTGGATC	TCATGGAGGC	CAACTCCCAG	780
TCGTGGACGC	CGATGCGCGA	GTCGTGGGGC	TCCATCTGGA	GGCTCGACTC	CAACCACCGC	840
CTCACGGCGC	CCTTCTCGCT	CCGCATCACC	AACGAGTCCG	GCAAGCAGCT	CGTCGCCAGC	900
CAGGTCATCC	CGGCCAACTG	GGCCCCCATG	GCCGTCTACC	GTTCTTTTCGT	CCAGTACAGC	960
AGCTAAGCCA	ATGATCAAGA	ACAAGCATAA	TTCATGCCTA	CTATAGCAGC	AGCAGAAGCA	1020
GCATTAGCTA	CTATACATAC	CTCTACGTAC	GACATTTGAG	ATCGATCGTT	TGGCCATTTT	1080
TATCTGCTCG	GGTATTGATT	AGCTCTCCCT	CGGTATTGTT	ATGGATTTGC	ATGGATGGTT	1140
CATTAATCTG	TCATCAGGAG	TTCGTTTTGA	GTAGGTGAGA	CGTCGGTTGT	TGGGTGTCAT	1200
ATAGACATCG	CTCGGTGTNT	TGAGGTTGAG	AGTGGGATAA	GGAGGAGGCA	AAGTTTGTCAT	1260
GTGCTGTCCC	GCCCACTCTC	ACTGTACCAG	TGTCACTGTT	TGTGTAACCA	GAACAAAGGT	1320
CATAAATTAT	ACTANTAGTA	TACAGTTTGC	TGCCTGGCNA	AAAAAAAAAN	AAAAANAA	1378

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACGCGCGTT	AATACGATCA	TATAGGGCGA	ATTGGGTACG	GGCCCCCCT	CGAGGTCGAC	60
CCACGCGTCC	GCACCGCCAC	CTCTCTCATC	GGATCCCTGC	ARAGGARAG	AGGGCAGTGG	120
CGGCGAAAGG	CGACATGGGC	TCGCTGTCCT	CTCTCGCCGC	CGCGGCGGTG	TTTCTCTCCC	180
TCCTCGCCGT	CGGCCACTGC	GCCGCCGCCG	ACTTCAGCGC	CACCGAYGCC	GACGCCGACT	240
TCGCCGGCAA	CGGCGTGGAC	TTCAACTCCA	GCGACGCCGC	CGTCTACTGG	GGCCCCCTGGA	300
CCAAGGCCAG	GGCCACCTGG	TACGGCCAGC	CCAACGGCGC	CGGCCCCGAC	GACAACGGCG	360
GCGCGTGCGG	GTTCAAGCAC	ACCAACCAGT	ACCCGTTTCAT	GTCGATGACC	TCCTGCGGCA	420

ACCAGCCATT	GTTCAAGGAC	GGCAAGGGAT	GCGGCTCTTG	CTACAAGATC	AGATGCACCA	480
AGGACCAGTC	CTGCTCCGGC	AGGTCGGANA	CGGTGATCAT	CACCGACATG	AACTACTWMC	540
CGGTGGCTCC	GTTCCACTTC	GACCTCAGCG	GCACGGCGTT	CGGCAGGCTC	GCCAASCYTG	600
GCCTCAACGA	CAAGCTGCGC	CACTCCGGCA	TCATCGACAT	CGAKTTCACC	ARGGTGCCAT	660
GCGAGTTCCC	GGGGCTCAAG	ATCGGGTTCC	ACGTGGAGGA	GTACTCGAAC	CCTGTGTACT	720
TCGCGGTGCT	GGTGGAGTAC	NAGGACGGCG	ACGGCGACGT	GGTGCAGGTG	GACCTGATGG	780
AGTCNAAACG	GCGCACGGGC	CGCCGACGGG	GGAGGTGGAC	GCCGATGAGG	GAGTCGTGGG	840
GSTCCATCTG	GAGGCTGGAC	ACCAACCACA	GGCTCCAGGC	CCCCTTYTCC	ATCCGCATCC	900
GCAACGAGTC	CGGCAAGACG	YTYGTCGCCA	ACAACGTCAT	CCCGGCCAAC	TGGAGGCCCA	960
ACACATTYTA	CCGCTCCTTC	GTCCAGTACA	GCTGAACCGC	CGCTCGCCGG	CGGCGACCCT	1020
CGGCGCCGGC	ATCGCCGCCG	CTGCTGCTGC	TAGTAATACT	ACTACTGCTA	TGATGTAATT	1080
GTGTTACCGG	TTGGGTTYTT	TGAGTTTGTT	GGGGTTGGGG	ATTGTGTGGT	CGGTCTGTGT	1140
TGCGATTTGC	AGAAACCGGG	CGARCGAAAG	AAGAAAAAAA	AAGCTGTKTK	GGAAATGGAG	1200
GAGGTAGGCG	TACAAGGTTA	CGCTTTCCCG	CCCACCTTCG	CTTTTATAAT	TTATCATTTT	1260
CAAATGGTGA	TGATATGATG	ATTAATCAAA	AGGATTATAT	TGCTAAAAAA	AAAAAAAAAA	1320
GGGCGGCCCG	CACCGCGGTG	GAGCTCCAGC	TTTTGTTCCC	TTTAGTGAGG	TTAATTGCGC	1380
GCTTGGGTAT	CA					1392

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AATCCCAGCT	ACCTAACCGA	TTGCCCAACA	AGAAAATAGC	AATGGTTAGC	CGGGGCACTT	60
TCGTTTTTGC	CGTCCTAGTG	GCGCTACCGA	TACTGTCACT	CCCCGTCTCT	GGCTACGAGC	120
AGAACTACAC	TGCCGGCAGA	CGGAGCACCA	TGTCGCTGGG	CAGAGGCTAC	GGCTGGTCCT	180
CCGGCGGGCG	GACGTGGTAC	GGCGGCCCGC	AAGGNGACGG	CAGCGAAGGT	GGCGCGTGCG	240
GTTACCAGAG	CGCCGTCGGG	CAGCGCCGTT	TCTCGTCGAT	GATCGCCGCC	GGGGGGCCCT	300
CCCTCTTCAA	GAATGGCAAA	GGCTGCGGCT	CATGCTACCA	AATTAAGTGC	ANCGGCAACC	360
GGGCGTTCTT	CGGCCGCCAG	TGACCGTCGT	GATCAACGAC	TTCTNCCCTT	GAGGGGTATT	420

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TACTTACTAC	CACTACTACT	GCTGCTGCTG	CCAGTTCTAG	CTAGCCTACT	GCTCTTCTCC	60
GAGCTGAAGA	TTTTTCGAGC	TAGCTAGGAT	GGCAGCCAGA	ATGGGCAGCA	AGGTCGCTGC	120
AATCCTCGCG	ATTCTGTCCG	TGCTCGTGGT	GCATGGCTCT	TGCAAGGGGC	ATCCTGTGAA	180
CTACAACGTC	TCCGACGCCT	CCGCCTACGG	CTCCGGCTGG	CTCCCTGCCC	GGGCAACCTG	210

GTATGGCGCT CCCACCGGCG CCGGCCCTGA CGGNNACAAC GGCGGCGCTT GCGGGGTTCA	300
AGAACGTGAA CCAGTACCCA TTCTCGTCCA TGACCTCCTN CGGAAACGAG CCCATTT	357

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGACAATTC TTGTCGTAGA TCGATACTAC ATGCTCATGA ACTTACTCTT TGCTCTAACT	60
TGTCTCCTCT TGAACCTAAC TCATTGCTTT AGCCCCAAGA AATTCAACAT TTCAGCCGCC	120
ACGACCAGCG ATTCTGATTG GTCTATCGCC GGATCTACGT GGTATGGTAA CCCCACCGGA	180
TACGGAAGCG ACGGTGGAGC TTGTGGTTAT GGAAATGCTG TTGCACAACC TCCGTTTTTCG	240
AAAATGGTAT CAGCCGGAGG TCCGTCGTTG TTCAAGTCAG GAAAAGGATG TGGTGATGT	300
TACCAGGTAA AATGCACTTC GAAATCGGCA TGTTCGAAAA ATCCTGTTAC GGTGGTCATT	360
ACAGATGAAT GTCCTGGATG CGTTAAGGAG TCGGTCCATT TCGATTGAG TGGTACAGCG	420
TTTGGTGCCA TGGCAATTTT TGGTCAAGAT AGTCAGCTTC GCAATGTCGG AGAATTGCAG	480
ATTCTTTATA AAAAGGTTGA GTGCAACTAT ATAGGCAAAA CCGTGACATT TCAAGTGGAT	540
AAAGGTTCAA ACGCTAACTC CTTGCGGGTT TTGGTTGCGT ATGTAAACGG AGACGGCGAA	600
ATTGGCCGAA TTGAACTCAA ACAAGCTCTA GATTCTGACA AGTGGTTGTC TATGAGCCAA	660
TCATGGGGCG CCGTGTGGAA GCTCGACGTG TCGTCACCTT TCGGTGCCCC GCTCTCTCTC	720
CGAGTGACTT CGTTGGAATC CGGCAAGACT GTTGTGGCTT CCAATGTCAT TCCCGCAAAC	780
TGGCAACCCG GTGCGATATA CAAATCCAAC GTCAACTTT	819

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 261 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Ala	Gly	Ala	Ser	Ala	Lys	Val	Val	Ala	Met	Leu	Leu	Ser	Val	Leu	
1					5					10						15
Ala	Thr	Tyr	Gly	Phe	Ala	Ala	Gly	Val	Val	Tyr	Thr	Asn	Asp	Trp	Leu	
20					25					30						
Pro	Ala	Lys	Ala	Thr	Trp	Tyr	Gly	Gln	Pro	Asn	Gly	Ala	Gly	Pro	Asp	
35								40					45			
Asp	Asn	Gly	Gly	Ala	Cys	Gly	Phe	Lys	Asn	Thr	Asn	Gln	Tyr	Pro	Phe	
50							55					60				
Met	Ser	Met	Thr	Ser	Cys	Gly	Asn	Glu	Pro	Leu	Phe	Gln	Asp	Gly	Lys	
65						70						75				80
Gly	Pro	Gly	Ala	Cys	Tyr	Gln	Ile	Arg	Cys	Thr	Asn	Asn	Pro	Ser	Cys	
85										90					95	
Ser	Gly	Gln	Pro	Arg	Thr	Val	Ile	Ile	Thr	Asp	Met	Asn	Tyr	Tyr	Pro	
100									105					110		
Val	Ala	Arg	Tyr	His	Phe	Asp	Leu	Ser	Gly	Thr	Ala	Phe	Gly	Ala	Met	
115							120						125			
Ala	Arg	Pro	Gly	Leu	Asn	Asp	Gln	Leu	Arg	His	Ala	Gly	Ile	Ile	Asp	
130						135						140				
Ile	Gln	Phe	Arg	Arg	Val	Pro	Cys	Tyr	His	Arg	Gly	Leu	Tyr	Val	Asn	
145										150					155	160
Phe	His	Val	Glu	Ala	Gly	Ser	Asn	Pro	Val	Tyr	Leu	Ala	Val	Leu	Val	
165										170					175	
Glu	Phe	Ala	Asn	Lys	Asp	Gly	Thr	Val	Val	Gln	Leu	Asp	Val	Met	Glu	
180							185						190			
Ser	Leu	Pro	Ser	Gly	Lys	Pro	Thr	Arg	Val	Trp	Thr	Pro	Met	Arg	Arg	
195							200						205			
Ser	Trp	Gly	Ser	Ile	Trp	Arg	Leu	Asp	Ala	Asn	His	Arg	Leu	Gln	Gly	
210						215					220					
Pro	Xaa	Ser	Leu	Arg	Met	Val	Ser	Glu	Ser	Gly	Gln	Thr	Val	Ile	Ala	
225							230								235	
240																
His	Gln	Val	Ile	Pro	Ala	Asn	Trp	Arg	Ala	Asn	Thr	Asn	Tyr	Gly	Ser	
245										250				255		
Lys	Val	Gln	Phe	Arg												
260																

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 295 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
Thr Arg Leu Tyr Asp His Ile Gly Glu Trp Val Arg Ala Pro Leu Glu
1           5           10           15
Val Asp Pro Arg Val Arg Gly Asp Val Glu Val Val Val Tyr Tyr Leu
20          25          30
Leu Leu Val Leu Val Val Val Gln Gly Cys Lys Gly Ser Ser Ala Val
35          40          45
Gln Gly Glu Gly Arg Trp Tyr Asn Glu Ser Glu Ala Ile Gly Gly Ala
50          55          60
Ala Ala Trp Gly Asn Ala Lys Ala Thr Trp Tyr Gly Gln Pro Asn Gly
65          70          75          80
Ala Gly Ala Ala Asp Asn Gly Gly Ala Cys Gly Phe Lys Lys Val Asn
85          90          95
Gln Tyr Pro Phe Met Gly Met Thr Ser Cys Gly Asn Xaa Pro Leu Tyr
100         105         110
Lys Gly Gly Lys Gly Cys Gly Ser Cys Tyr Arg Val Arg Cys Asn Arg
115         120         125
Asn Pro Ala Cys Ser Gly Asn Ala Gln Thr Val Ala Ile Xaa Asp Met
130         135         140
Asn Tyr Phe Pro Leu Ser Gln Tyr His Phe Asp Leu Ser Gly Ile Ala
145         150         155         160
Phe Gly Arg Leu Ala Lys Pro Gly Arg Ala Asp Asp Leu Arg Arg Ala
165         170         175
Gly Ile Ile Asp Val Gln Phe Ala Arg Val Pro Cys Glu Phe Pro Gly
180         185         190
Leu Lys Val Gly Phe His Val Glu Gly Ser Ser Pro Val Tyr Leu
195         200         205
Ala Val Leu Val Glu Tyr Glu Asn Gly Asp Gly Asp Val Ala Gln Val
210         215         220
Asp Leu Lys Glu Ala Gly Ala Gly Gly Gly Arg Trp Thr Pro Met Arg
225         230         235         240
Glu Ser Trp Gly Ser Val Trp Arg Leu Asp Ser Asn His Arg Leu Arg
245         250         255
Ala Pro Phe Ser Ile Arg Ile Arg Ser Asp Ser Gly Lys Thr Leu Val
260         265         270
Ala Pro Asp Val Ile Pro Leu Asn Trp Thr Pro Asn Thr Phe Tyr Arg
275         280         285
Ser Phe Val Gln Tyr Ser Ser
290         295
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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Gly Ala Ser Ala Lys Val Val Ala Met Leu Leu Ser Val Leu

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1           5           10           15
Ala Thr Tyr Gly Phe Ala Ala Gly Val Val Tyr Thr Asn Asp Trp Leu
20           25           30
Pro Ala Lys Ala Thr Trp Tyr Gly Gln Pro Asn Gly Ala Gly Pro Asp
35           40           45
Asp Asn Gly Gly Ala Cys Gly Phe Lys Asn Thr Asn Gln Tyr Pro Phe
50           55           60
Met Ser Met Thr Ser Cys Gly Asn Glu Pro Leu Phe Gln Asp Gly Lys
65           70           75           80
Gly Cys Gly Ala Cys Tyr Gln Ile Arg Cys Thr Asn Asn Pro Ser Cys
85           90           95
Ser Gly Gln Pro Arg Thr Val Ile Ile Thr Asp Met Asn Tyr Trp Pro
100          105          110
Val Ala Arg Tyr His Phe Asp Leu Ser Gly Thr Ala Phe Gly Ala Met
115          120          125
Ala Arg Pro Gly Leu Asn Asp Gln Leu Arg His Ala Gly Ile Ile Asp
130          135          140
Ile Gln Phe Arg Arg Val Pro Cys Tyr His Arg Gly Leu Tyr Val Asn
145          150          155          160
Phe His Val Glu Ala Gly Ser Asn Pro Val Tyr Leu Ala Val Leu Val
165          170          175
Glu Phe Ala Asn Lys Asp Gly Thr Val Val Gln Leu Asp Val Met Glu
180          185          190
Ser Leu Pro Ser Gly Lys Pro Thr Arg Val Trp Thr Pro Met Arg Arg
195          200          205
Ser Trp Gly Ser Ile Trp Arg Leu Asp Ala Asn His Arg Leu Gln Gly
210          215          220
Pro Ser Leu Arg Met Val Ser Glu Ser Gly Gln Thr Val Ile Ala His
225          230          235          240
Gln Val Ile Pro Ala Asn Trp Arg Ala Asn Thr Asn Tyr Gly Ser Lys
245          250          255
Val Gln Phe Arg
260

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(2) INFORMATION FCR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Met Gly Ser Leu Ser Ser Leu Ala Ala Ala Val Phe Leu Ser Leu
1           5           10           15
Leu Ala Val Gly His Cys Ala Ala Ala Asp Phe Asn Ala Thr Asp Ala
20           25           30
Asp Ala Asp Phe Ala Gly Asn Gly Val Asp Phe Asn Ser Ser Asp Ala
35           40           45
Ala Val Tyr Trp Gly Pro Trp Thr Lys Ala Arg Ala Thr Trp Tyr Gly
50           55           60
Gln Pro Asn Gly Ala Gly Pro Asp Asp Asn Gly Gly Ala Cys Gly Phe
65           70           75           80

```





(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
Met Ala Ala Arg Met Gly Ser Lys Val Ala Ala Ile Leu Ala Ile Leu
1           5           10           15
Ser Val Leu Val Val His Gly Ser Cys Lys Gly His Pro Val Asn Tyr
20          25          30
Asn Val Ser Asp Ala Ser Ala Tyr Gly Ser Gly Trp Leu Pro Ala Arg
35          40          45
Ala Thr Trp Tyr Gly Ala Pro Thr Gly Ala Gly Pro Asp Gly Xaa Asn
50          55          60
Gly Gly Ala Cys Gly Val Gln Glu Arg Glu Pro Val Pro Ile Leu Val
65 70 75 80
His Asp Leu Leu Arg Lys Arg Ala His Phe
85                      90
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
Met Ala Leu Thr Leu Gln Arg Ala Leu Ser Glu Leu Leu Thr Leu Ile
1           5           10           15
Ala Ile Leu Ser Ile Phe Leu Val Ile Pro Ser Phe Cys Phe Asn Pro
20          25          30
Lys Lys Leu Tyr Asn Ala Ser Tyr Tyr Ser Pro Ser Ser Ser Asp Trp
35          40          45
Ser Pro Ala Val Ala Thr Trp Tyr Gly Pro Ala Asn Gly Asp Gly Ser
50          55          60
Glu Gly Gly Ala Cys Gly Tyr Gly Asn Ala Val Gly Gln Pro Pro Phe
65 70 75 80
Ser Ser Leu Ile Ser Ala Gly Ser Pro Leu Ile Tyr Asp Ser Gly Gly
85          90          95
Lys Gly Cys Gly Ser Cys Glu Val Lys Cys Thr Gly Asn Ser Ala Cys
100         105         110
Ser Gly Asn Pro Val Lys Val Val Ile Thr Asp Glu Cys Ala Gly Cys
115         120         125
Gly Ser Asp Ala Gln Tyr His Phe Asp Leu Ser Gly Asn Ala Phe Gly
130         135         140
```

Ala Met Ala Ile Ile Gly Gln Asp Glu Asn Leu Arg Asn Ala Gly Lys	145	150	155	160
Ile Asn Ile Gln His Arg Arg Ile Glu Cys Asn Tyr Pro Gly Arg Ser	165	170	175	
Ile Ala Phe His Val Asp Ser Gly Ser Asn Gln Glu Tyr Phe Ala Thr	180	185	190	
Leu Val Glu Tyr Glu Asp Gly Asp Gly Asp Leu Leu Ala Lys Glu Leu	195	200	205	
Lys Glu Ala Leu Asp Ser Gly Ser Trp Asp Ser Met Gln Gln Ser Trp	210	215	220	
Gly Ala Val Trp Lys Phe Asp Lys Gly Ser Pro Leu Arg Ala Pro Phe	225	230	235	240
Ser Ile Lys Leu Thr Thr Leu Glu Ser Gly Gln Thr Ile Val Ala Asn	245	250	255	
Asn Asn Val Ile Pro Ala Trp Thr Pro Gly Gln Thr Tyr Arg Ser Ile	260	265	270	
Val Asn Phe Ala Thr	275			

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Thr Ile Leu Val Val Asp Arg Tyr Tyr Met Leu Met Asn Leu Leu	1	5	10	15	
Phe Ala Leu Thr Cys Leu Leu Leu Asn Leu Thr His Cys Phe Ser Pro	20	25	30		
Lys Lys Phe Asn Ile Ser Ala Ala Thr Thr Ser Asp Ser Asp Trp Ser	35	40	45		
Ile Ala Gly Ser Thr Trp Tyr Gly Asn Pro Thr Gly Tyr Gly Ser Asp	50	55	60		
Gly Gly Ala Cys Gly Tyr Gly Asn Ala Val Ala Gln Pro Pro Phe Ser	65	70	75	80	
Lys Met Val Ser Ala Gly Gly Pro Ser Leu Phe Lys Ser Gly Lys Gly	85	90	95		
Cys Gly Ala Cys Tyr Gln Val Lys Cys Thr Ser Lys Ser Ala Cys Ser	105				
Lys Asn Pro Val Thr Val Val Ile Thr Asp Glu Cys Pro Gly Cys Val	115	120	125		
Lys Glu Ser Val His Phe Asp Leu Ser Gly Thr Ala Phe Gly Ala Met	130	135	140		
Ala Ile Ser Gly Gln Asp Ser Gln Leu Arg Asn Val Gly Glu Leu Gln	145	150	155	160	
Ile Leu Tyr Lys Lys Val Glu Cys Asn Tyr Ile Gly Lys Thr Val Thr	165	170	175		
Phe Gln Val Asp Lys Gly Ser Asn Ala Asn Ser Phe Ala Val Leu Val	185	190			
Ala Tyr Val Asn Gly Asp Gly Glu Ile Gly Arg Ile Glu Leu Lys Gln					

195	200	205	
	Ala Leu Asp Ser Asp Lys Trp Leu Ser Met Ser Gln Ser Trp Gly Ala		
210	215	220	
	Val Trp Lys Leu Asp Val Ser Ser Pro Leu Arg Ala Pro Leu Ser Leu		
	225	230	235
	Arg Val Thr Ser Leu Glu Ser Gly Lys Thr Val Val Ala Ser Asn Val		240
	245	250	255
	Ile Pro Ala Asn Trp Gln Pro Gly Ala Ile Tyr Lys Ser Asn Val Asn		
	265	270	
	Phe		
	□		